AMENDMENTS TO THE SPECIFICATION

Amend the paragraph beginning at page 10, line 31, as follows:

The tRNA genes were identified using the tRNA-SCAN program (Fichant, G. A., *et al., J Mol Biol,* **220**:659-71 (1991)) and the rRNA genes were identified using the BLASTN program (Altschul, S. F., *et al., Nucleic Acids Res,* **25**:3389-402 (1997)) with archaeal rRNA as search queries. For the identification of the protein-coding genes, the genome sequence was conceptually translated in 6 frames to generate potential protein products of open reading frames (ORFs) longer than 100 codons (from stop to stop). These potential protein sequences were compared to the database of Clusters of Orthologous Groups (COGs) of proteins using COGNITOR (Tatusov, R. L., *et al., Science,* **278**:631-7 (1997)). After manual verification of the COG assignments and selection of start sites, the validated COG members from *M. kandleri* were considered protein-coding genes. The COG assignment procedure was repeated for ORF products greater than 60 codons obtained from the intergenic regions. Other potential protein sequences were compared to the non-redundant (NR) protein sequence database using the BLASTP program and to a six-frame translation of unfinished microbial genomes using the TBLASTN program. Those that produced hits with E (expectation) values <0.01 were added to the protein set after an examination of the alignments. Finally, protein-coding regions were predicted using the GeneMarkS (Besemer, J., *et al., Nucleic Acids Res.* **29**:2607-18 (2001)) and SYNCOD (Rogozin, I. B.,. *et al., Gene,* **226**:129-37 (1999)) programs. The genes predicted with these methods in the regions between evolutionarily conserved genes were added to produce the final protein set. (See Attachment B SEQ ID ~~Nos.; 1-1691)~~ NOS. 1-1688 and 1690-1692.)